

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 11, 2003, 01:56:12 ; Search time 22 Seconds
(without alignments)
203.611 Million cell updates/sec

Title: US-09-914-324A-1
Perfect score: 616
Sequence: 1 MAAMADVTPSGTNSGAGK.....KTRQVCPIDNREMEFOXYGH 108

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	209	33.9	84	AN11_MOUSE	Q9CPX9 mus musculus
2	208	33.8	84	AN11_HUMAN	Q9N9Y5 homo sapien
3	91	14.8	148	RN24_HUMAN	Q9Y225 homo sapien
4	90	14.6	600	RN12_MOUSE	Q9WLV7 mus musculus
5	88	14.3	161	Y0UD_CAEEL	P30631 caenorhabdi
6	87	14.1	624	RN12_HUMAN	Q9N9W2 homo sapien
7	86	14.0	326	PEXA_HUMAN	O60683 homo sapien
8	83.5	13.6	115	YBR2_YEAST	P38239 saccharomyc
9	83	13.5	685	RNF6_HUMAN	Q9Y252 homo sapien
10	82.5	13.4	532	ICP0_HSVB	P28990 equine herp
11	80	13.0	284	GOLI_DROME	O06003 drosophila
12	79.5	12.9	796	PRH_AYATH	P48785 arabidopsis
13	79	12.8	381	RN13_CHICK	Q90972 gallus gall
14	79	12.8	381	RN13_HUMAN	O43567 homo sapien
15	79	12.8	410	ICP0_PVIF	P29129 pseudorabie
16	79	12.8	1680	FUR2_DROME	P30432 drosophila
17	78.5	12.7	235	Y057_CAEEL	Q09463 caenorhabdi
18	78	12.7	381	RN13_MOUSE	O54965 mus musculus
19	77	12.5	279	SLI3_HUMAN	Q14192 homo sapien
20	77	12.5	295	PEXA_PICAN	Q00940 pichia angu
21	76.5	12.4	758	YKDA_YEAST	P36096 saccharomyc
22	76	12.3	1493	M3K1_YEAST	P53349 mus musculus
23	76	12.3	1493	M3K1_RAT	O62825 rattus norv
24	76	12.3	1493	M3K1_HUMAN	O13333 homo sapien
25	75.5	12.3	676	ICP0_HSVB1	P29128 bovine herp
26	75.5	12.3	676	ICP0_HSVB2	P29128 bovine herp
27	74.5	12.1	825	ICP0_HSV2H	P28284 herpes simp
28	74	12.0	474	CHIC_HUMAN	O9U184 homo sapien
29	73.5	11.9	485	RNF8_HUMAN	O76064 homo sapien
30	73.5	11.9	486	RNF8_MOUSE	O8V056 mus musculus
31	72.5	11.8	416	YHR5_YEAST	P38823 saccharomyc
32	72.5	11.8	775	ICP0_HSV11	P08393 herpes simp
33	70.5	11.4	337	PEXA_YEAST	Q05568 saccharomyc

34	70.5	11.4	342	ME18_MOUSE	P23798 mus musculus
35	70.5	11.4	344	ME18_HUMAN	P35227 homo sapien
36	70.5	11.4	467	ICP0_VZVD	O09309 varicella-z
37	70.5	11.4	585	YH80_YEAST	P38748 saccharomyc
38	70.5	11.4	610	Y0DA_CAEEL	O09268 caenorhabdi
39	70.5	11.4	1562	YMB1_YEAST	O04781 saccharomyc
40	70.5	11.4	2569	LMN3_MOUSE	O61789 mus musculus
41	69.5	11.3	1238	Y009_CAEEL	O09282 caenorhabdi
42	69	11.2	353	REON_HUMAN	Q92782 homo sapien
43	69	11.2	397	REON_MOUSE	P56163 rattus norv
44	69	11.2	507	MK3_HUMAN	O13064 homo sapien
45	69	11.2	564	YUES_CAEEL	P90859 caenorhabdi

ALIGNMENTS

RESULT 1	AN11_MOUSE	STANDARD:	PRT:	84 AA.
ID	AN11_MOUSE			
AC	Q9CPX9:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Anaphase promoting complex subunit 11.			
GN	ANAPC11.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Embryo;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi Y., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,			
RA	Kuhei P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombearts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Williams L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,			
RA	Hayashizaki Y.,			
RT	"Functional annotation of a full-length mouse cDNA collection."			
RL	Nature 409:685-690(2001).			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
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CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL; AK003612; BAB22890.1; -			
CC	EMBL; AK003244; BAB22663.1; -			
CC	MGI; MGI:1913406; Anapc11.			
CC	InterPro: IPR001841; Znf_ring.			
CC	SMART; SM00184; RING_1.			
CC	PROSITE; PS00518; ZF_RING_1; FALSE_NBS.			
CC	PROSITE; PS50089; ZF_RING_2; 1.			
CC	Zinc-finger.			
CC	34 77 RING-TYPE.			
CC	FT			


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DR EMBL: BC000213; AAH00213.1; -
DR EMBL: AL079313; CAB45279.1; -
DR HSSP: P28990; 1CHC.
DR Genew: HGNC:13779; RNF24.
DR InterPro: IPR001841; Znf_finger.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
KM Zinc-finger.
FT ZN_FING 78 119 RING-TYPE.
FT CONFLICT 45 45 Y->S (IN REF. 3).
SO SEQUENCE 148 AA; 17209 MW; 66C240CA35991EA5 CRC64;

Query Match 14.8%; Score 91; DB 1; Length 148;
Best Local Similarity 58.3%; Pred. No. 0.0032;
Matches 14; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 75 CNHAFHFCISRWLKTROYCPILDN 98
Db | |||| | : ||| : 1: |||| |
96 CKHAFHRCILIKMLVRRVCPCLN 119

RESULT 4
RN12.MOUSE STANDARD; PRT; 600 AA.
ID RN12_MOUSE
AC Q9WTV7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RING finger protein 12 (LIM domain interacting RING finger protein)
DE (RING finger LIM domain-binding protein) (R-LIM).
GN RNF12 OR RLIM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090.
RN [1]
RA BACH I.;
RA BACH I.;
RT "Opposing developmental functions of positive and negative
RT coregulators of LIM homeodomain factors.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
RN [2]
RP FUNCTION.
RX MEDLINE=99364422; PubMed=10431247;
RA Bach I., Rodriguez-Esteban C., Carriere C., Bhushan A., Krones A.,
RA Rose D.W., Glass C.K., Andersen B., Izpisua Belmonte J.C.,
RA Rosenfeld M.G.;
RT "RLIM inhibits functional activity of LIM homeodomain transcription
RT factors via recruitment of the histone deacetylase complex.";
RL Nat. Genet. 22:394-399(1999).
CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN
CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE
CC DEACETYLASE COREPRESSOR COMPLEX.
CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -----
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CC -----
CC EMBL: AF069992; AAD34209.1; -
DR MGD: MGI:1342291; Rnf12.
DR InterPro: IPR001841; Znf_finger.
DR Pfam: PF00097; Zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE: PS50089; ZF_RING_2; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.

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KW      Transcription regulation; Zinc-finger.
FT      DOMAIN          415    484        SER-RICH.
FT      ZN_FING         546    587        RING-TYPE.
FT      DOMAIN          447    461        POLY-SER.
SO      SEQUENCE       600 AA; 66470 MW; E68299530126E4ID CRC64;

Query Match              14.6%; Score 90; DB 1; Length 600;
Best Local Similarity   52.0%; Pred. No. 0.017;
Matches 13; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

OY      75 CNHAFHCISRMTKTQVCPDNR 99
Db      564 CSHEFHVCHDRMLSENSTCPCRR 588
               ||| |||| |
               ||| |||| |

RESULT 5
YOU_D_CAEEL STANDARD; PRT; 161 AA.
AC AC     P30631;
DT DT      01-APR-1993 (Rel. 25, Created)
DT DT      01-OCT-1993 (Rel. 27, Last sequence update)
DT DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE DE      Hypothetical 18.8 KDa protein ZK637.14 in chromosome IIT.
GN GN      ZK637.14.
OS OS      Caenorhabditis elegans.
OC OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
CC CC      Rhabdilitidae; Peloderinae; Caenornabdtitis.
CX CX      NCBI_Taxid=6239;
RN RN      [1]
RP RP      SEQUENCE FROM N.A.
RC RC      STRAIN=Bristol NZ;
RX RX      MEDLINE=92168156; PubMed=1538779;
RA RA      Sulston J., Du Z., Thomas K., Wilson R., Hillier L., Staden R.,
RA Hailtson N., Green P., Thierry-Mieg J., Olu L., Dear S., Coulson A.,
RA Craxton M., Durbin R., Berks M., Metzstein M., Hawkins T.,
RA Alnconough R., Waterston R.;
RL RL      "Nature C. elegans genome sequencing project: a beginning.";
RT RT      Article 356:37-41(1992).
CC CC      -I SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC CC      -----
CC CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC      -----
DR DR      EMBL; Z11115; CAAT7447.1; -.
DR DR      PIR; S15788; S15788.
DR DR      WormPep; ZK637.14; CE00432.
DR DR      InterPro; IPR001841; Zn_fing.
DR DR      Pfam; PF00097; zf-C3HC4; 1.
DR DR      SMART; SM00184; RING_1.
DR DR      PROSITE; PS00518; ZE_RING_1; FALSE_NEG.
DR DR      Hypothetical protein; zinc-finger.
KW KW      ZN_FING             72    134        RING-TYPE.
FT FT      SEQUENCE       161 AA; 18847 MW; FSEFP93A83AGC027 CRC64;

Query Match              14.3%; Score 88; DB 1; Length 161;
Best Local Similarity   31.1%; Pred. NO. 0.0075;
Matches 19; Conservative 12; Mismatches 22; Indels 8; Gaps 2;

OY      42 CATCRNHIM-----DLCLICQANQAASASECTVANGVCNHAHFHCISRMFKTROVC 94
DB      72 CATCDNDNNVDIEDHVIK-EELKDIPDTFGTTIVVPCKHRPHFCLTFLMLEAQOTC 130
OY      95 P 95
DB      131 P 131

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OY 3 AAMDVDPSTGNSGAGKRRFEVKWNAVALMWDIVDNCALCRHNDLCECOANQAS 62
 DB 104 AAKMIPKTKG-----KESDEK-----DLSDSCAIC-----IE 131
 OY 63 ATSECTVAMGVCNNAHFHCISRWLKTROVCP 96
 DB 132 AYKPTDTRILPCCKHEFRKNCIDPWLIEHRCPM 165

RESULT 12
 PRH_ARATH STANDARD: PRT: 796 AA.
 AC P48785;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pathogenesis-related homeodomain protein (PRHA).
 GN PRH OR PRHA OR AT4G2940 OR F27B13.180.
 OS Arabidopsis thaliana. (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 OX [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC MEDLINE=94312876; PubMed=7913642;
 RX MEDLINE=94312876; PubMed=7913642;
 RA Korfage U., Trezzini G.F., Meier I., Hahlbrock K., Somssich I.E.;
 RT "Plant homeodomain protein involved in transcriptional regulation of
 a pathogen defense-related gene";
 RL Plant Cell 6:695-708(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC MEDLINE=98012533; PubMed=9351248;
 RX MEDLINE=98012533; PubMed=9351248;
 RA Mayer K.F.X., Schueller C., Wambolt R., Murphy G., Volckaert G.,
 RT Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
 RA Harris B., Ansoorge W., Brandt P., Griwall L.A., Rieger M.,
 RA Welcheslgerter M., de Simone V., Obermaier B., Maché R., Meier M.,
 RA Kreis M., Delseny M., Pulgomech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohnsels J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Biham L., Robben J.,
 RA Van der Schueren J., Grymoprez B., Chuang Y.-J., Vandennusche F.,
 RA Breken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
 RA Weltzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moolljman P., Klein Lankhorst R., Rose M., Hauf J., Kottler P.,
 RA Bernerster S., Hempel S., Feldpausch M., Lambers S., Van den Daale H.,
 RA De Keyser A., Buysnaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark U., Doggett J., Hall S., Kay M., Lennard N., Mcay K., Mayes R.,
 RA Petelt A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borikova D., Boecker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fattmann B., Grandrath K., Dunner D., Herzl A.,
 RA Neumann S., Argitau D., Vitale D., Liguori R., Piravandi E.,
 RA Massenet O., Quigley F., Clabaud G., Wendelin A., Feilber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aboung S.,
 RA Chetoui F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielek C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegler L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stokking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Granat E., Shohdy N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
 RA Chen E., Maria M., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana";
 RL Nature 402:769-777(1999).
 CC -I- FUNCTION: SPECIFICALLY BINDS TO THE FUNGAL ELICITOR-RESPONSIVE
 CC DNA ELEMENT, 5'-CTATTGTTA-3', OF THE GENE PR2 PROMOTER.
 CC -I- SUBCELLULAR LOCATION: Nuclear.
 CC -I- INDUCTION: BY PATHOGEN INFECTION.
 CC -I- SIMILARITY: BELONGS TO THE PHD-ASSOCIATED HOMEBOX FAMILY.
 CC -I- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
 CC -I- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
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 DR EMBL: L21991; AAA32843.1; -;
 DR EMBL: U48864; AAC49836.1; -;
 DR EMBL: AL050352; CAB43669.1; -;
 DR EMBL: AL161575; CAB79752.1; -;
 DR TRANSFAC: T04108; -;
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR001965; Znf-PHD.
 DR Pfam: PF006428; homeobox.1.
 DR Pfam: PF00628; PHD.1.
 DR Prodom: PD000010; Homeobox.1.
 DR SMART: SM00389; HOX.1.
 DR SMART: SM00249; PHD.1.
 DR PROSITE: PS50071; HOMEBOX_2; 1.
 DR PROSITE: PS50139; ZF-PHD_1; 1.
 DR PROSITE: PS50016; ZF-PHD_2; 1.
 KW Homeobox; DNA-binding; Nuclear protein; Transcription regulation;
 KW Repeat; Zinc-finger.
 FT ZN_FING 190 247 PHD-TYPE.
 FT DOMAIN 294 303 ASP-RICH (ACIDIC).
 FT DNA_BIND 452 511 HOMEBOX.
 FT DOMAIN 605 735 5 X 27 AA TANDEM REPEATS.
 FT REPEAT 605 631 1.
 FT REPEAT 632 658 2.
 FT REPEAT 659 685 3.
 FT REPEAT 686 712 4.
 FT REPEAT 713 735 5 (INCOMPLETE).
 FT DOMAIN 738 759 LEUCINE-ZIPPER.
 SQ SEQUENCE 796 AA; 90657 MW; 5E61509A0CADB175 CRC64;

Query Match 12.9%; Score 79.5; DB 1; Length 796;
 Best Local Similarity 29.5%; Pred. No. 0.34;
 Matches 18; Conservative 12; Mismatches 26; Indels 3; Gaps 2;

OY *37 IVDNCALCRHNDLCECOANQASATSECTVAMGVCNNAHFHCISRWLKTROVCP 96
 DB 179 VIASDGSIHNDH--FCACNRSREA-FPNDNITLDCGTGNRAFHOKCLDPLETESIPG 235
 OY 97 D 97
 DB 236 D 236

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RESULT 13
RN13_CHICK
ID RN13_CHICK STANDARD: PRT; 381 AA.
AC Q90972;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RING finger protein 13 (C-RZF).
GN RN13 OR RZF.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Brain;
RX MEDLINE=96181541; PubMed=8610176;
RA Triangue P., Crossin K.L., Cirilli C., Edelman G.M., Mauro V.P.;
RT "Identification and characterization of a RING zinc finger gene
(C-RZF) expressed in chicken embryo cells."
RL Proc. Natl. Acad. Sci. U.S.A. 93:3105-3109(1996).
RN [2]
RP TISSUE SPECIFICITY.
RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
RT "The gene for a RING zinc finger protein is expressed in the inner
chick ear after noise exposure."
RL Prim. Sens. Neuron 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed primarily in brain and heart.
CC Also expressed in inner ear after noise exposure.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC
DR EMBL; X93455; CA64725.1; -.
DR InterPro: IPR000561; EGF-1like.
DR InterPro: IPR003137; PA.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam; PF00067; ZF-C3HC4; 1.
DR Pfam; PF02225; PA; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR ZN_FINGER; Nuclear protein.
FT ZN_FINGER 240
FT SEQUENCE 381 AA; 42819 MW; 661615C4033C6A CRC64;
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Query Match 12.8%; Score 79; DB 1; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.18;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;
QY 40 DNCAICRHHMDLCTEQANQASATSECTYAMGVCHNAHFHCISRWL-KTRQVCPL 96
Db 238 DVCALCDEYED-----GDKLRILP-PCSHAYHCCKVDPMWTKTKKCPV 280
ID RN13_HUMAN STANDARD: PRT; 381 AA.
AC O43567;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE RING finger protein 13.
GN RNF13 OR RZF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
RC TISSUE=Brain;
RX MEDLINE=96181541; PubMed=8610176;
RA Triangue P., Crossin K.L., Cirilli C., Edelman G.M., Mauro V.P.;
RT "Identification and characterization of a RING zinc finger gene
(C-RZF) expressed in chicken embryo cells."
RL Proc. Natl. Acad. Sci. U.S.A. 93:3105-3109(1996).
RN [2]
RP TISSUE SPECIFICITY.
RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
RT "The gene for a RING zinc finger protein is expressed in the inner
chick ear after noise exposure."
RL Prim. Sens. Neuron 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed primarily in brain and heart.
CC Also expressed in inner ear after noise exposure.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR Pfam; PF02225; PA; 1.
DR SMART; SM00184; RING; 1.
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DR PROSITE; PS00089; ZF_RING_2; 1.
DR ZN_FINGER; Nuclear protein.
FT ZN_FINGER 240
FT SEQUENCE 381 AA; 42819 MW; 661615C4033C6A CRC64;
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Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;
QY 40 DNCAICRHHMDLCTEQANQASATSECTYAMGVCHNAHFHCISRWL-KTRQVCPL 96
Db 238 DVCALCDEYED-----GDKLRILP-PCSHAYHCCKVDPMWTKTKKCPV 280
ID RN13_HUMAN STANDARD: PRT; 381 AA.
AC O43567;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
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RX MEDLINE=96181541; PubMed=8610176;
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RP TISSUE SPECIFICITY.
RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
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RL Prim. Sens. Neuron 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed primarily in brain and heart.
CC Also expressed in inner ear after noise exposure.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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DR EMBL; X93455; CA64725.1; -.
DR InterPro: IPR000561; EGF-1like.
DR InterPro: IPR003137; PA.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam; PF00067; ZF-C3HC4; 1.
DR Pfam; PF02225; PA; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR ZN_FINGER; Nuclear protein.
FT ZN_FINGER 240
FT SEQUENCE 381 AA; 42819 MW; 661615C4033C6A CRC64;
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Best Local Similarity 29.3%; Pred. No. 0.18;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3;
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Db 238 DVCALCDEYED-----GDKLRILP-PCSHAYHCCKVDPMWTKTKKCPV 280
ID RN13_HUMAN STANDARD: PRT; 381 AA.
AC O43567;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
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RA Triangue P., Crossin K.L., Cirilli C., Edelman G.M., Mauro V.P.;
RT "Identification and characterization of a RING zinc finger gene
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RL Proc. Natl. Acad. Sci. U.S.A. 93:3105-3109(1996).
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RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
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chick ear after noise exposure."
RL Prim. Sens. Neuron 2:305-316(1998).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Expressed primarily in brain and heart.
CC Also expressed in inner ear after noise exposure.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC
DR EMBL; X93455; CA64725.1; -.
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DR InterPro: IPR003137; PA.
DR InterPro: IPR001841; ZnF_Ring.
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DR Pfam; PF02225; PA; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS00089; ZF_RING_2; 1.
DR ZN_FINGER; Nuclear protein.
FT ZN_FINGER 240
FT SEQUENCE 381 AA; 42819 MW; 661615C4033C6A CRC64;
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Query Match 12.8%; Score 79; DB 1; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.18;
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Db 238 DVCALCDEYED-----GDKLRILP-
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OC Homo sapiens (Human).
OC Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homininae;
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Lomax M.I., Warner S.J., Bersirli C.G., Gong T.-W.L.;
RT "the gene for a RING zinc finger protein is expressed in the inner
RT chick ear after noise exposure.";
RL prim. Sens. Neuron 2:305-316(1998).
RN (2)
RP SEQUENCE FROM N.A.
RA Yu W., Glibbs R.A.;
RC TISSUE=Brain.
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Brain, and urinary bladder.
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
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CC
CC EMBL; AF037204; AAC03769.1; -
CC EMBL; AF070558; AAC28641.1; -
CC EMBL; BC009803; AAH09803.1; -
CC EMBL; BC009781; AAH09781.1; -
CC Genew: HGNC:10057; RNF13.
CC InterPro: IPR001317; PA.
CC InterPro: IPR001841; Znf_ring.
CC Pfam: PF00097; zf-C3HC4; 1.
CC Pfam: PF02225; PA; 1.
CC SMART: SM00184; RING; 1.
CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
CC PROSITE: PS50089; ZF_RING_2; 1.
CC Zinc-finger; Nuclear protein.
CC ZN_FING 240 282
CC FT
CC SQ SEQUENCE 381 AA; 4500727D0F197653 CRC64;
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Query Match 12.8%; Score 79; DB 1; Length 381;
Best Local Similarity 29.3%; Pred. No. 0.18;
Matches 17; Conservative 10; Mismatches 15; Indels 16; Gaps 3.
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Db 238 DVCATCDEYED-----GDKRRL-PCSHAYHKCKVDPMYTKTKKTCVP 280

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RT      "Cloning of the latency gene and the early protein 0 gene of
RT      pseudorabies virus."
RL      J. Virol. 65:5260-5271(1991).
CC      -|- FUNCTION: MAY BE A GENERAL TRANSACTIVATOR WHICH FUNCTIONS
CC      SYNERGISTICALLY WITH IE180. IT MAY PLAY A ROLE IN THE REACTIVATION
CC      OF LATENT PRV.
CC      -|- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC      -|- SIMILARITY: TO OTHER HERPESVIRUSES ICPO PROTEIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M57504; AAA47463.1; -.
DR      HSSP: P28990; ICHC.
DR      InterPro: IPR001841; znf_fing.
DR      Pfam: PF00097; zf-C3HC4; 1.
DR      SMART: SM00184; RING; 1.
DR      PROSITE: PS00518; ZF_RING_1; 1.
DR      PROSITE: PS50089; ZF_RING_2; 1.
KW      Transcription regulation; Trans-acting factor; Activator; Zinc-finger;
KW      DNA-binding; Early protein.
FT      ZN_FING 46 85
FT      ZN_FING 85
SQ      SEQUENCE 410 AA; 43838 MW; E35384FE86F82D11 CRC64;
      RING-TYPE.

Query Match      12.8%; Score 79; DB 1; Length 410;
Best Local Similarity 21.7%; Pred. No. 0.19;
Matches 18; Conservative 5; Mismatches 20; Indels 40; Gaps 1;

OY      56 COANQASATSECTVAMGV-----C 75
DB      3 CTVSRRTTAAESSAMGIFGYRPSPPQRLSLPLTVMDCPICLDVAAATEAQTLP 62
OY      76 NHAHFHCISRWLKTROVCPIDN 98
DB      63 MHKFCIDCIORWTLTSTACPLCN 85

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Search completed: May 11, 2003, 02:10:04
 Job time : 25 secs

